#2

OIPE

RAW SEQUENCE LISTING DATE: 05/08/2001
PATENT APPLICATION: US/09/838,028 TIME: 15:55:54

Input Set : A:\00125US2.ST25.txt
Output Set: N:\CRF3\05082001\I838028.raw

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      3 <110> APPLICANT: Lind, Peter
      4       Berthold, Malin
      6 <120> TITLE OF INVENTION: Novel G Protein-Coupled Receptor
      8 <130> FILE REFERENCE: 00125US2
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/838,028
C--> 10 <141> CURRENT FILING DATE: 2001-04-19
     10 <150> PRIOR APPLICATION NUMBER: 60/198,600
     11 <151> PRIOR FILING DATE: 2000-04-19
     13 <160> NUMBER OF SEQ ID NOS: 12
     15 <170> SOFTWARE: PatentIn version 3.0
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 1540
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Homo sapiens
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     27 atcagggaac tcttccactt tggggagggt ccctcaaacc ccaggtccct ctactgccag    180
     29 tggggtcccg gaggtggggc tacgggatgt tgcttcggaa tctgtggccc tcttcttcat    240
     31 gctcctgctg gacttgactg ctgtggctgg caatgccgct gtgatggccg tgatcgccaa    300
     33 gacgcctgcc ctccgaaaat ttgtcttcgt cttccacctc tgcctggtgg acctgctggc    360
     35 tgccctgacc ctcatgcccc tggccatgct ctccagctct gccctctttg accacgccct    420
     37 ctttggggag gtggcctgcc gcctctactt gtttctgagc gtgtgctttg tcagcctggc    480
     39 catcctctcg gtgtcagcca tcaatgtgga gcgctactat tacgtagtcc accccatgcg    540
     41 ctacgaggtg cgcatgacgc tggggctggt ggcctctgtg ctggtgggtg tgtgggtgaa    600
     43 ggccttggcc atggcttctg tgccagtgtt gggaagggtc tcctgggagg aaggagctcc    660
     45 cagtgtcccc ccaggctgtt cactccagtg gagccacagt gcctactgcc agctttttgt    720
     47 ggtggtcttt gctgtccttt actttctgtt gcccctgctc ctcatacttg tggtctactg    780
     49 cagcatgttc cgagtggccc gcgtggctgc catgcagcac gggccgctgc ccacgtggat    840
     51 ggagacaccc cggcaacgct ccgaatctct cagcagccgc tccacgatgg tcaccagctc    900
     53 gggggccccc cagaccaccc cacaccggac gtttgggggа gggaaagcag cagtggttct    960
     55 cctggctgtg gggggacagt tcctgctctg ttggttgccc tacttctctt tccacctcta   1020
     57 tgttgccctg agtgctcagc ccatttcaac tgggcaggtg gagagtgtgg tcacctggat   1080
     59 tggctacttt tgcttcactt ccaacccttt cttctatgga tgtctcaacc ggcagatccg   1140
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     63 gctgcctagc cgggagggct ccattgagga gaacttcctg cagttccttc aggggactgg   1260
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     67 tgttgacttt cgaatcccag gccagatagc tgaggagacc tctgagttcc tggagcagca   1380
     69 actcaccagc gacatcatca tgtcagacag ctacctccgt cctgccgcct caccccggct   1440
     71 ggagtcatga tgggccgctg gacactcgga gggatatggg gctggggcca gttatgattg   1500
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     78 <212> TYPE: PRT
     79 <213> ORGANISM: Homo sapiens
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84 1               5                  10                  15
86 Gly Arg Val Pro Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro
87             20                  25                  30
89 Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
90         35                  40                  45
92 Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
93     50                  55                  60
95 Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
96 65                  70                  75                  80
98 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
99                 85                  90                  95
101 Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
102            100                 105                 110
104 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
105        115                 120                 125
107 Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val
108    130                 135                 140
110 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
111 145                 150                 155                 160
113 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
114                165                 170                 175
116 Pro Val Leu Gly Arg Val Ser Trp Glu Glu Gly Ala Pro Ser Val Pro
117            180                 185                 190
119 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
120        195                 200                 205
122 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile
123    210                 215                 220
125 Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met
126 225                 230                 235                 240
128 Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser
129                245                 250                 255
131 Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro
132            260                 265                 270
134 Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val
135        275                 280                 285
137 Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
138    290                 295                 300
140 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
141 305                 310                 315                 320
143 Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
144                325                 330                 335
146 Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
147            340                 345                 350
149 Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Glu Leu
150        355                 360                 365
152 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
153    370                 375                 380
155 Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu
156 385                 390                 395                 400
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Input Set : A:\00125US2.ST25.txt
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159                 405                 410                 415
161 Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser
162             420                 425                 430
164 Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg
165         435                 440                 445
167 Leu Glu Ser
168     450
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 1909
172 <212> TYPE: DNA
173 <213> ORGANISM: Rattus norvegicus
175 <400> SEQUENCE: 3
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178 aacaggaagt gccctgggtg tccttttteg gccccatgga gtcctcaccc atcccccagt    120
180 catcaggaaa ctcatccact ttgggaaggg cccttcaaac cccaggtccc tctacggcca    180
182 gcggagtccc agagttggga ctaagggacg tggcttcgga atctgtggcc ctcttcttca    240
184 tgcttctgtt ggatctcact gctgtggcgg gcaatgctgc tgtgatggct gttattgcca    300
186 agacacccgc cctccgaaag tttgtttttg tcttccatct ctgtctggtg gacctgctgg    360
188 ctgccctgac cctcatgccc ctggccatgc tctccagctc tgccctcttt gaccacgccc    420
190 tctttgggga ggtggcctgc cgcctctacc tgttcctgag cgtttgcttt gtcagcctgg    480
192 ccatcctttc ggtgtctgcc attaatgtgg agcgctacta ttatgtggtc caccccatgc    540
194 gctacgaggt gcgcatgaca ctagggctgg tggcctctgt gctggtgggc gtgtgggtaa    600
196 aggccctggc catggcgtct gtgccagtgt tgggaagggt ctactgggag gaaggagctc    660
198 ccagtgttaa cccaggctgt tctctccaat ggagccatag tgcctactgc cagcttttg     720
200 tggtggtctt tgctgttctt tacttcttgc tgcccttgat cctgatcttt gtggtctact    780
202 gcagcatgtt tcgagtggct cgcgtggctg ccatgcaaca tgggccgctg cccacgtgga    840
204 tggagacgcc ccggcaacgc tctgagtctc tcagtagccg ctctactatg gtcactagct    900
206 ccggggctca tcagaccacc ccacaccgga cgtttggggg tgggaaggca gcagtggtcc    960
208 tcctggctgt cgggggacag ttcttgcttt gttggttacc ctacttctct ttccatctct   1020
210 atgttgccct gagcgctcag cccatttcaa caggacaggt ggagaatgtg gtgacctgga   1080
212 tcggctactt ttgcttcact tccaaccctt ttttctatgg atgtctcaac cgtcagatcc   1140
214 ggggcgagct tagcaaacag tttgtctgtt tcttcaaggc agctccagag gaggagctga   1200
216 ggctgccgag tcgcgagggc tccatcgagg agaatttcct acagtttctc cagggtacat   1260
218 ctgagaactg ggtttctcgg cccctaccca gccctaagcg ggagccaccg cctgctgttg   1320
220 actttcgaat cccaggccag attgctgagg agacctcgga gttcttggag cagcaactca   1380
222 ccagcgacat catcatgtcg gacagctacc tccgtcctgc cccttcacca aggctggagt   1440
224 catgatggac agacactagg agggaataag gcttggggct ggtttatcat ctcaaggatt   1500
226 gcttttccag ctggctgggg tttggactcg ggtctctgga cttagctttt gtgtggtgtt   1560
228 tcctgggtca ggaccagagt caacgggatg gacatgtggc aaaaagcctt ggacttggct   1620
230 gtgatctttg actattgggg gagggatcct gggtatggtg agacggtgat gagagaaaag   1680
232 ggtgacaaag gtgagggaaa gcctttctac cagtgaactc ttcgtgcctc aggagacagg   1740
234 gcaacttctg ggtaggcatt ggagcagcag gctaggagca gttattctgg ggaccgttga   1800
236 ggtttacttc tttccagtgt catagtccag actaatattt atactgagac aaggtaagaa   1860
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241 <210> SEQ ID NO: 4
242 <211> LENGTH: 449
243 <212> TYPE: PRT
244 <213> ORGANISM: Rattus norvegicus
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Input Set : A:\00125US2.ST25.txt
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251 Gly Arg Ala Leu Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro
252 20 25 30
254 Glu Leu Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
255 35 40 45
257 Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
258 50 55 60
260 Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
261 65 70 75 80
263 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
264 85 90 95
266 Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
267 100 105 110
269 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
270 115 120 125
272 Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val
273 130 135 140
275 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
276 145 150 155 160
278 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
279 165 170 175
281 Pro Val Leu Gly Arg Val Tyr Trp Glu Glu Gly Ala Pro Ser Val Asn
282 180 185 190
284 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
285 195 200 205
287 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Ile Leu Ile
288 210 215 220
290 Phe Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met
291 225 230 235 240
293 Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser
294 245 250 255
296 Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala His
297 260 265 270
299 Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val
300 275 280 285
302 Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
303 290 295 300
305 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
306 305 310 315 320
308 Gln Val Glu Asn Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
309 325 330 335
311 Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
312 340 345 350
314 Ser Lys Gln Phe Val Cys Phe Phe Lys Ala Ala Pro Glu Glu Glu Leu
315 355 360 365
317 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
318 370 375 380

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Input Set : A:\00125US2.ST25.txt
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320 Leu Gln Gly Thr Ser Glu Asn Trp Val Ser Arg Pro Leu Pro Ser Pro
321 385                 390                 395                 400
323 Lys Arg Glu Pro Pro Pro Ala Val Asp Phe Arg Ile Pro Gly Gln Ile
324                 405                 410                 415
326 Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser Asp Ile
327             420                 425                 430
329 Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Pro Ser Pro Arg Leu Glu
330         435                 440                 445
332 Ser
335 <210> SEQ ID NO: 5
336 <211> LENGTH: 25
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <223> OTHER INFORMATION: Primer
345 <400> SEQUENCE: 5
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350 <211> LENGTH: 25
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial Sequence
354 <220> FEATURE:
355 <221> NAME/KEY: misc_feature
356 <223> OTHER INFORMATION: Primer
359 <400> SEQUENCE: 6
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365 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <221> NAME/KEY: misc_feature
370 <223> OTHER INFORMATION: Primer
373 <400> SEQUENCE: 7
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378 <211> LENGTH: 48
379 <212> TYPE: DNA
380 <213> ORGANISM: Artificial Sequence
382 <220> FEATURE:
383 <221> NAME/KEY: misc_feature
384 <223> OTHER INFORMATION: Primer
387 <400> SEQUENCE: 8
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391 <210> SEQ ID NO: 9
392 <211> LENGTH: 18
393 <212> TYPE: DNA
394 <213> ORGANISM: Artificial Sequence
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VERIFICATION SUMMARY DATE: 05/08/2001
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Input Set : A:\00125US2.ST25.txt
Output Set: N:\CRF3\05082001\I838028.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date